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Amino acid alignment

- 1 *M. incognita* MDH1
- 2 *M. incognita* MDH2
- 3 *C. elegans* MDH1
- 4 *C. elegans* MDH2

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      .10      .20      .30      .40      .50      .60
1 .....MNY.....KDAPEFVVS PKDAREFVVK: 23
2 .....MNY.....KDAPEFVVS PKDAREFVVK: 23
3 .....MTIKDKREFNETDEI VISKEKLDSEVLE: 28
4 MELLQRALVFTGGHISRYQAVIAVNSVGKNARFYSTTDDMAAPEESVVAKDEM KREME: 60

      .70      .80      .90      .100     .110     .120
1 CMQTVGTSPDHA GQLADLLLDADLVGHYSHGLRLRLHIYVD DVKNG.VKGNNGVEKVLKQKG: 82
2 CMQTVGTSPDHA GQLADLLLDADLVGHYSHGLRLRLHIYVD DVKNG.VKGNNGVEKVLKQKG: 82
3 CLAKAGCTGDHA GQLADLLLDADLVGHYSHGLRLRLHIYVD DVKNG.VKGNNGVEKVLKQKG: 88
4 CMTKVGATESHA TQLALVLEEDIRGHYSHGLRLRLDMIVRDI EQNVCKGDGEPIILKERA:120

      .130     .140     .150     .160     .170     .180
1 GTARVDGEMLLGAVVGNEFC TDLAIKLAKKEFGVAWVUTENS NHYGACQHYTKKIANAGMVG:142
2 GTARVDGEMLLGAVVGNEFC TDLAIKLAKKEFGVAWVUTENS NHYGACQHYTKKIANAGMVG:142
3 STARVDGEMLLGAVVGNEFC TDLAIKLAKKEFGVAWVUTENS NHYGACQHYTKKIANAGMVG:148
4 GTARVDGEMLLGAVVGNEFC TDLAIKLAKKEFGVAWVUTENS NHYGACQHYTKKIANAGMVG:180

      .190     .200     .210     .220     .230     .240
1 MSFTTSPIMFPCRSSEIGLGTPLSCCVNSEKTGDSFLDMATTTVALGKVELADCRGK:202
2 MSFTTSPIMFPCRSSEIGLGTPLSCCVNSEKTGDSFLDMATTTVALGKVELADCRGK:202
3 MSFTTSPIMFPCRSSEIGLGTPLSCCVNSEKTGDSFLDMATTTVALGKVELADCRGK:207
4 MSFTTSPIMFPCRSSEIGLGTPLSCCVNSEKTGDSFLDMATTTVALGKVELADCRGK:238

      .250     .260     .270     .280     .290     .300
1 TQIPSTWGADSKGNPSTDTQVVLHGGGLLPLGGIEETGSGYKGTGLSMMGELFCGILAGSS:262
2 TQIPSTWGADSKGNPSTDTQVVLHGGGLLPLGGIEETGSGYKGTGLSMMGELFCGILAGSS:262
3 TQIPSTWGADSKGNPSTDTQVVLHGGGLLPLGGIEETGSGYKGTGLSMMGELFCGILAGSS:267
4 NPVPLSNGVGECKETDTPTKVLYGGGLLPLGGIEETGSGYKGTGLSMMGELFCGILAGSS:298

      .310     .320     .330     .340     .350     .360
1 EGKIVRLWGQSHKAADNGQCFVAIDQECFAPGFAPRLQQLDETRELKPISEEEKPVLPVG:322
2 EGKIVRLWGQSHKAADNGQCFVAIDQECFAPGFAPRLQQLDETRELKPISEEEKPVLPVG:322
3 EGKIVRLWGQSHKAADNGQCFVAIDQECFAPGFAPRLQQLDETRELKPISEEEKPVLPVG:327
4 WCPHVRKRMSTKSEADNGQCFVAIDQECFAPGFAPRLQQLDETRELKPISEEEKPVLPVG:358

      .370     .380     .390     .400
1 DEERMNTEYSQKAGGLVYQEGQIKAFEEELATKCDVQMFSYKRLK.:366
2 DEERMNTEYSQKAGGLVYQEGQIKAFEEELATKCDVQMFSYKRLK.:366
3 DEERAHNMCDLGGIVYKKRQLDHEKFNADRLGVIMRLVDEKPPQ:372
4 DMERRHEALVEQLGGIPYHKNQITFVNDLAAKLGKTVDLVQ...:400

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FIG. 3